Fragmentation of N-Linked Carbohydrates with Q-Trap and ToF-ToF Mass Spectrometers

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Summary

1. Neutral acetylation was used for the carbohydrate precursors to be measured as the sodium adducts. A Q-Trap mass spectrometer was employed in the negative ion mode to allow conjugate ion measurements.
2. The neutral mass spectra produced from each ion were used to determine the fragment ions associated with the ion. The mass spectrometer was operated in the collision cell to increase the signal-to-noise ratio of the fragment ions.
3. The results of the fragmentation experiments were compared with those obtained from other mass spectrometers, including a ToF-ToF instrument. The fragmentation patterns were consistent between the different mass spectrometers.

Methods

Sample preparation

1. Neutral acetylation was used for the carbohydrate precursors to be measured as the sodium adducts. A Q-Trap mass spectrometer was employed in the negative ion mode to allow conjugate ion measurements.
2. The neutral mass spectra produced from each ion were used to determine the fragment ions associated with the ion. The mass spectrometer was operated in the collision cell to increase the signal-to-noise ratio of the fragment ions.
3. The results of the fragmentation experiments were compared with those obtained from other mass spectrometers, including a ToF-ToF instrument. The fragmentation patterns were consistent between the different mass spectrometers.

Results and Discussion

Q-Trap

1. Negative ion spectra of the neutral carbohydrate adducts were obtained from a Q-Trap mass spectrometer. The spectra contained mainly cross-ring cleavage fragments, with some evidence of C-type glycosidic cleavages.
2. The negative ion spectra were compared with those obtained from other mass spectrometers, including a ToF-ToF instrument. The fragmentation patterns were consistent between the different mass spectrometers.

MS² Spectra

1. MS² spectra were obtained by collision-induced dissociation of the ionized carbohydrate precursors. The spectra contained mainly cross-ring cleavage fragments, with some evidence of C-type glycosidic cleavages.
2. The MS² spectra were compared with those obtained from other mass spectrometers, including a ToF-ToF instrument. The fragmentation patterns were consistent between the different mass spectrometers.

Negative ion spectra

1. Negative ion spectra of the neutral carbohydrate adducts were obtained from a Q-Trap mass spectrometer. The spectra contained mainly cross-ring cleavage fragments, with some evidence of C-type glycosidic cleavages.
2. The negative ion spectra were compared with those obtained from other mass spectrometers, including a ToF-ToF instrument. The fragmentation patterns were consistent between the different mass spectrometers.

ToF-ToF high energy spectra

1. ToF-ToF high energy spectra of the neutral carbohydrate adducts were obtained from a ToF-ToF mass spectrometer. The spectra contained mainly cross-ring cleavage fragments, with some evidence of C-type glycosidic cleavages.
2. The ToF-ToF high energy spectra were compared with those obtained from other mass spectrometers, including a Q-Trap instrument. The fragmentation patterns were consistent between the different mass spectrometers.

Conclusions

1. The results of the fragmentation experiments were consistent between the different mass spectrometers. This suggests that the fragmentation patterns are reliable and can be used to identify the carbohydrate structures.
2. The fragmentation patterns were similar to those obtained from other mass spectrometers, including a ToF-ToF instrument. This suggests that the fragmentation patterns are consistent across different mass spectrometers.

References


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